



1600

## RAW SEQUENCE LISTING

DATE: 06/05/2003

PATENT APPLICATION: US/09/495,448A

TIME: 11:15:37

Input Set : A:\50111301\_1.TXT

Output Set: N:\CRF4\06052003\I495448A.raw

3 <110> APPLICANT: LAU, Lester F.  
 5 <120> TITLE OF INVENTION: EXTRACELLULAR MATRIX SIGNALLING MOLECULES  
 7 <130> FILE REFERENCE: 28758/36072  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/495,448A  
 C--> 10 <141> CURRENT FILING DATE: 2000-01-31  
 12 <150> PRIOR APPLICATION NUMBER: 09/142,569  
 13 <151> PRIOR FILING DATE: 1999-04-02  
 15 <150> PRIOR APPLICATION NUMBER: 60/013,958  
 16 <151> PRIOR FILING DATE: 1996-03-15  
 18 <160> NUMBER OF SEQ ID NOS: 34  
 20 <170> SOFTWARE: PatentIn Ver. 2.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1480  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Mus musculus  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (180)..(1316)  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: Mouse cyr61 cDNA coding sequence  
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 37 aaggacaccc gccgcctcgg ccctgcgctc accgcactcc gggcgcatctt gatcccgctg 120  
 39 ctgcgcgggt tgttggttct gtgtgcgcgc gctgcgcccg gttctctctg cgcgccaca 179  
 41 atg agc tcc agc acc ttc agg acg ctc gct gtc gcc gtc acc ctt ctc 227  
 42 Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu  
 43 1 5 10 15  
 45 cac ttg acc aga ctg gcg ctc tcc acc tgc ccc gcc gcc tgc cac tgc 275  
 46 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys  
 47 20 25 30  
 49 cct ctg gag gca ccc aag tgc gcc ccg gga gtc ggg ttg gtc cgg gac 323  
 50 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
 51 35 40 45  
 53 ggc tgc ggc tgc tgt aag tgc gct aaa caa ctc aac gag gac tgc 371  
 54 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
 55 50 55 60  
 57 agc aaa act cag ccc tgc gac cac acc aag ggg ttg gaa tgc aat ttc 419  
 58 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
 59 65 70 75 80  
 61 ggc gcc agc tcc acc gct ctg aaa ggg atc tgc aga gct cag tca gaa 467  
 62 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
 63 85 90 95  
 65 ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa agc 515

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66 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
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69 ttc cag ccc aac tgt aaa cac cag tgc aca tgt att gat ggc gcc gtg 563
70 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
71          115          120          125
73 ggc tgc att cct ctg tgt ccc caa gaa ctg tct ctc ccc aat ctg ggc 611
74 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
75          130          135          140
77 tgt ccc aac ccc cgg ctg gtg aaa gtc agc ggg cag tgc tgt gaa gag 659
78 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
79 145          150          155          160
81 tgg gtt tgt gat gaa gac agc att aag gac tcc ctg gac gac cag gat 707
82 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
83          165          170          175
85 gac ctc ctc gga ctc gat gcc tcg gag gtg gag tta acg aga aac aat 755
86 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
87          180          185          190
89 gag tta atc gca att gga aaa ggc agc tca ctg aag agg ctt cct gtc 803
90 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
91          195          200          205
93 ttt ggc acc gaa ccg cga gtt ctt ttc aac cct ctg cac gcc cat ggc 851
94 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
95          210          215          220
97 cag aaa tgc atc gtt cag acc acg tct tgg tcc cag tgc tcc aag agc 899
98 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
99 225          230          235          240
101 tgc gga act ggc atc tcc aca cga gtt acc aat gac aac cca gag tgc 947
102 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
103          245          250          255
105 cgc ctg gtg aaa gag acc cgg atc tgt gaa gtg cgt cct tgt gga caa 995
106 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
107          260          265          270
109 cca gtg tac agc agc cta aaa aag ggc aag aaa tgc agc aag acc aag 1043
110 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
111          275          280          285
113 aaa tcc cca gaa cca gtc aga ttt act tat gca gga tgc tcc agt gtc 1091
114 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
115          290          295          300
117 aag aaa tac cgg ccc aaa tac tgc ggc tcc tgc gta gat ggc cgg tgc 1139
118 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
119 305          310          315          320
121 tgc aca cct ctg cag acc aga act gtg aag atg cgg ttc cga tgc gaa 1187
122 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
123          325          330          335
125 gat gga gag atg ttt tcc aag aat gtc atg atg atc cag tcc tgc aaa 1235
126 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
127          340          345          350
129 tgt aac tac aac tgc ccg cat ccc aac gag gca tcg ttc cga ctg tac 1283
130 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr

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131          355          360          365
133 agc cta ttc aat gac atc cac aag ttc agg gac taagtgcctc cagggttcct 1336
134 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
135          370          375
137 agtgtgggct ggacagagga gaagcgcaag catcatggag acgtgggtgg gcgaggatg 1396
139 aatgggtgcct tgctcattct tgagtagcat tagggatattt caaaactgcc aaggggctga 1456
141 tgtggacgga cagcagcgca gccg 1480
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145 <211> LENGTH: 379
146 <212> TYPE: PRT
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151 1 5 10 15
153 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
154 20 25 30
156 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
157 35 40 45
159 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
160 50 55 60
162 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
163 65 70 75 80
165 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
166 85 90 95
168 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
169 100 105 110
171 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
172 115 120 125
174 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
175 130 135 140
177 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
178 145 150 155 160
180 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
181 165 170 175
183 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
184 180 185 190
186 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
187 195 200 205
189 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
190 210 215 220
192 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
193 225 230 235 240
195 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
196 245 250 255
198 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
199 260 265 270
201 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
202 275 280 285
204 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val

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205      290      295      300
207 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
208 305      310      315      320
210 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
211      325      330      335
213 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
214      340      345      350
216 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
217      355      360      365
219 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
220      370      375
223 <210> SEQ ID NO: 3
224 <211> LENGTH: 1418
225 <212> TYPE: DNA
226 <213> ORGANISM: Homo sapiens
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (124)..(1266)
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Human cyr61 cDNA coding sequence
235 <400> SEQUENCE: 3
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238 tgcacaccag cttgttggcg tcttcgtcgc cgcgctcgcc ccgggctact cctgcgcgcc 120
240 aca atg agc tcc cgc atc gcc agg gcg ctc gcc tta gtc gtc acc ctt 168
241 Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
242 1 5 10 15
244 ctc cac ttg acc agg ctg gcg ctc tcc acc tgc ccc gct gcc tgc cac 216
245 Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
246 20 25 30
248 tgc ccc ctg gag gcg ccc aag tgc gcg ccg gga gtc ggg ctg gtc cgg 264
249 Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
250 35 40 45
252 gac ggc tgc ggc tgc tgt aag gtc tgc gcc aag cag ctc aac gag gac 312
253 Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
254 50 55 60
256 tgc agc aaa acg cag ccc tgc gac cac acc aag ggg ctg gaa tgc aac 360
257 Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
258 65 70 75
260 ttc ggc gcc agc tcc acc gct ctg aag ggg atc tgc aga gct cag tca 408
261 Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
262 80 85 90 95
264 gag ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa 456
265 Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
266 100 105 110
268 agt ttc cag ccc aac tgt caa cat cag tgc aca tgt att gat ggc gcc 504
269 Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
270 115 120 125
272 gtg ggc tgc att cct ctg tgt ccc caa gaa cta tct ctc ccc aac ttg 552
273 Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu

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277	Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu			
278	145 150 155			
280	gag tgg gtc tgt gac gag gat agt atc aag gac ccc atg gag gac cag	648		
281	Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln			
282	160 165 170 175			
284	gac ggc ctc ctt ggc aag gag ctg gga ttc gat gcc tcc gag gtg gag	696		
285	Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu			
286	180 185 190			
288	ttg acg aga aac aat gaa ttg att gca gtt gga aaa ggc aga tca ctg	744		
289	Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu			
290	195 200 205			
292	aag cgg ctc cct gtt ttt gga atg gag cct cgc atc cta tac aac cct	792		
293	Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro			
294	210 215 220			
296	tta caa ggc cag aaa tgt att gtt caa aca act tca tgg tcc cag tgc	840		
297	Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys			
298	225 230 235			
300	tca aag acc tgt gga act ggt atc tcc aca cga gtt acc aat gac aac	888		
301	Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn			
302	240 245 250 255			
304	cct gag tgc cgc ctt gtg aaa gaa acc cgg att tgt gag gtg cgg cct	936		
305	Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro			
306	260 265 270			
308	tgt gga cag cca gtg tac agc agc ctg aaa aag ggc aag aaa tgc agc	984		
309	Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser			
310	275 280 285			
312	aag acc aag aaa tcc ccc gaa cca gtc agg ttt act tac gct gga tgt	1032		
313	Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys			
314	290 295 300			
316	ttg agt gtg aag aaa tac cgg ccc aag tac tgc ggt tcc tgc gtg gac	1080		
317	Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp			
318	305 310 315			
320	ggc cga tgc tgc acg ccc cag ctg acc agg act gtg aag atg cgg ttc	1128		
321	Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe			
322	320 325 330 335			
324	cgc tgc gaa gat ggg gag aca ttt tcc aag aac gtc atg atg atc cag	1176		
325	Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln			
326	340 345 350			
328	tcc tgc aaa tgc aac tac aac tgc ccg cat gcc aat gaa gca gcg ttt	1224		
329	Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe			
330	355 360 365			
332	ccc ttc tac agg ctg ttc aat gac att cac aaa ttt agg gac	1266		
333	Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp			
334	370 375 380			
336	taaagtctac ctgggtttcc agggcacacc tagacaaaca agggagaaga gtgtcagaat	1326		
338	cagaatcatg gagaaaatgg gcgggggtgg tgtgggtgat gggactcatt gtagaaagga	1386		
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**VERIFICATION SUMMARY**

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Input Set : A:\50111301\_1.TXT

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date